

SEQUENCE LISTING

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<110> Svendsen, Allan
      Minning, Stefan

<120> Protease Variants

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<170> PatentIn version 3.3

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Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
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Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
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Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
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Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
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Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
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Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
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Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
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Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
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 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
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25 30 35

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Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
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Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
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Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
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atc aat aca ggt gcg agc caa tat gat ttt gcc gtg atc aaa aca gat Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp 90 95 100			576
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 Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
 155 160 165

gga aat tca ggc tca gcg atg cta gat caa aat cag caa att gtt ggg 816
 Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
 170 175 180

gtt cat aac gca ggg tat tca aac ggt acg att aat ggc ggt cca aaa 864
 Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
 185 190 195 200

gcg aca gct gcc ttt gtt gaa ttt atc aac tat gca aaa gcg caa 909
 Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
 205 210 215

<210> 8
 <211> 303
 <212> PRT
 <213> *Esacillus pumilus* B032

<400> 8

Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
 -85 -80 -75

Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu
 -70 -65 -60

Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
 -55 -50 -45

Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
 -40 -35 -30 -25

Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
 -20 -15 -10

Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg
 -5 -1 1 5

Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
 10 15 20

Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
 25 30 35 40

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
45 50 55

Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 9
<211> 954
<212> DNA
<213> Bacillus licheniformis CDJ31

<220>
<221> CDS
<222> {1}..(954)

<220>
<221> sig_peptide
<222> {1}..(84)

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<220>
<221> pro_peptide
<222> {85}..{288}

<220>
<221> mat_peptide
<222> {259}..{954}

<400> 9
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Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
      -95                      -90                      -85

tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tgc ccg      96
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80                      -75                      -70                      -65

cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca      144
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
      -60                      -55                      -50

agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa      192
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
      -45                      -40                      -35

gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa      240
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
      -30                      -25                      -20

agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa      288
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
      -15                      -10                      -5                      -1

tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca      336
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
1                      5                      10                      15

tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc      384
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
      20                      25                      30

acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc      432
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
      35                      40                      45

att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct      480
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
      50                      55                      60

ccg gga ggg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc      528
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
65                      70                      75                      80

cgc tat ttc atc ccg tca gcc tat cga agc gga aat tgc aat tac gac      576
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
      85                      90                      95

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tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat	624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr	
100 105 110	

ttc gga tat tcc tac acc acc tcg tct ctc gtt ggg tca agc gtt acc	672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr	
115 120 125	

atc atc gga tat cca ggc gac aaa aca tcg ggc acc caa tgg cag atg	720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met	
130 135 140	

tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc	768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile	
145 150 155 160	

gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc	816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser	
165 170 175	

tcc aga ccg aat tgc agc ggc cca tgt tcg ctg gcc gtt cat acg aat	864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn	
180 185 190	

ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa	912
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys	
195 200 205	

gaa gta ttc gat aat ttg aca aac tgg aaa sac agc gcc caa	954
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln	
210 215 220	

<210> 10
 <211> 318
 <212> PRT
 <213> Bacillus licheniformis CDJ31

<400> 10

Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile	
-95 -90 -85	

Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro	
-80 -75 -70 -65	

His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala	
-60 -55 -50	

Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys	
-45 -40 -35	

Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
-30 -25 -20

Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
-15 -10 -5 -1

Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
1 5 10 15

Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
20 25 30

Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
35 40 45

Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
50 55 60

Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
65 70 75 80

Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
85 90 95

Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
100 105 110

Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
115 120 125

Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
130 135 140

Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
145 150 155 160

Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser
165 170 175

Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn
180 185 190

Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys

Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 210 215 220

<210> 11
 <211> 906
 <212> DNA
 <213> *Escherichia coli* JA96

<220>
 <221> CDS
 <222> {1}..(906)

<220>
 <221> sig_peptide
 <222> {1}..(75)

<220>
 <221> pro_peptide
 <222> {76}..(261)

<220>
 <221> mat_peptide
 <222> {262}..(906)

<400> 11
 atg aaa aag gtg aaa aaa tta atc cct tct cta ctc gtt ttt ggt gct 48
 Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
 -85 -80 -75

tta agt gtg cct agt ttt gcc cat gca gca tct gat tca gta ctt acg 96
 Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
 -70 -65 -60

tct gat tat gac atg gtg act tct gac gga aag gtg att tct tca gct 144
 Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40

gac ttc cac aac gat atg aaa acc ccc tca tcc ttt gac aaa gtg gat 192
 Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25

gat ctc tct tct act att ggc gaa aaa gta aaa cca ctc aca aca tat 240
 Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10

tta aaa gac ttt caa aca aaa gta gtc att gga gac gat ggt aga aca 288
 Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5

aaa gtg acg aat aca aga gta gca ccc tat aat tct att gct tat att 336
 Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25

aca ttt ggt gga tct agc tgc act gga aca ctc att gct cca aac aaa Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys 30 35 40	384
ata ttg aca aac gga cac tgc gtc tac aat aca gcc aca aga agt tat Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr 45 50 55	432
agt gca aaa ggg tct gtc tac cca ggc atg aat gac agc acg gct gtg Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val 60 65 70	480
aac ggc tca gca aac atg acc gaa ttc tat gta cca agc gga tat atc Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile 75 80 85	528
aac acg ggg gcg agt caa tat gat ttt gcc gtc att aaa aca gat acg Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr 90 95 100 105	576
aac att gga aat acg gtc ggc tat cgc tct att cgt caa gtg aca aat Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn 110 115 120	624
cta aca ggt aca acg att aaa att tct gga tat cca ggt gat aaa atg Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met 125 130 135	672
aga tcg act gcc aaa gtg tca caa tgg gaa atg tca ggt cca gtc acg Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr 140 145 150	720
aga gaa gat acg aat ctc gca tac tat acg atc gat aca ttt agc gga Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly 155 160 165	768
aac tct gcc tct gcg atg cta gat cag aac caa caa atc gtc ggg gtc Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val 170 175 180 185	816
cat aat gcg ggt tat tca aat gga acg atc aac ggt gga cca aaa gcg His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala 190 195 200	864
act gct gcc ttt gtt gaa ttt atc aac tat gcg aag gcg caa Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln 205 210 215	906

<210> 12
 <211> 302
 <212> FRT
 <213> Bacillus pumilus JA96
 <400> 12

Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
-85 -80 -75

Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
-70 -65 -60

Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
-55 -50 -45 -40

Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
-35 -30 -25

Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
-20 -15 -10

Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
-5 -1 1 5

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
10 15 20 25

Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
30 35 40

Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
45 50 55

Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
60 65 70

Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
75 80 85

Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
90 95 100 105

Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
110 115 120

Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
125 130 135

Arg Ser Thr Gly Lys Val Ser Gln Tip Glu Met Ser Gly Pro Val Thr

140

145

150

Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
 155 160 165

Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
 170 175 180 185

His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
 190 195 200

Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
 205 210 215

<210> 13

<211> 939

<212> DNA

<213> Bacillus subtilis IS75

<220>

<221> CDS

<222> (1)..(939)

<220>

<221> sig_peptide

<222> (1)..(102)

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<222> (103)..(279)

<220>

<221> mat_peptide

<222> (280)..(939)

<400> 13

atg aaa tta gtt cca aga ttc aga aaa caa tgg ttc gct tac tta acg 48
 Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr
 -90 -85 -80

gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca 96
 Val Leu Cys Leu Ala Leu Ala Ala Val Ser Phe Gly Val Pro Ala
 -75 -70 -65

aaa gcg gca gag aac ccg caa act tct gta tgg aat acc ggt aaa gaa 144
 Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
 -60 -55 -50

gct gat gct acg aaa aac caa acg tca aaa gca gat cag gtt tcc gcc 192
 Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
 -45 -40 -35 -30

cct tat gag gga acc gga aaa aca agt aaa tcg tta tac ggc ggc caa Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln -25 -20 -15	240
acg gaa ctg gaa aaa aac att caa acc tta cag cct tcg agc att atc Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile -10 -5 -1 1	288
gga act gat gaa cgc acc aga atc tcc agc acg aca tct ttt cca tat Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr 5 10 15	336
aga gca acc gtt caa ctg tca atc aag tat ccc aac act tca agc act Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr 20 25 30 35	384
tat gga tgt acc gga ttt tta gtc aat cca aat aca gtc gtc acg gct Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala 40 45 50	432
gga cat tgt gtg tac agc cag gat cat gga tgg gct tcg acg ata acc Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr 55 60 65	480
gcc gcg cgc ggc cgc aat ggt tcg tca tat cgg tac ggt act tat tca Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser 70 75 80	528
ggc acg atg ttt tac tcc gtc aaa gga tgg acg gaa agc aaa gac acc Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr 85 90 95	576
aac tat gat tac gga gct att aaa tta aac ggt tct cct gga aac acg Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr 100 105 110 115	624
gtt ggc tgg tac ggc tac cgg act aca aac agc agc agt ccc gtg ggc Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly 120 125 130	672
ctt tcc tcg tca gtg aca gga ttc cca tgt gac aaa acc ttt ggc acg Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr 135 140 145	720
atg tgg tct gat aca aag cgg att cgc tcc gct gaa acg tat aag ctg Met Trp Ser Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu 150 155 160	768
acc tat aca acc gat acg tac ggc tgc caa agc ggc tcg cct gtt tat Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr 165 170 175	816
cga aac tac agt gat aca ggg cag aca gct att gcc att cac acg aac Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn 180 185 190 195	864

gga gga tgg tca tat aac ttg gga sca agg gtg acg aac gat gta ttc 912
 Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
 200 205 210

aac aat att caa tat tgg gca aat caa 939
 Asn Asn Ile Gln Tyr Trp Ala Asn Gln
 215 220

<210> 14
 <211> 313
 <212> PRT
 <213> Bacillus subtilis IS75

<400> 14

Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr
 -90 -85 -80

Val Leu Cys Leu Ala Leu Ala Ala Ala Val Ser Phe Gly Val Pro Ala
 -75 -70 -65

Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu
 -60 -55 -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
 -45 -40 -35 -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
 -25 -20 -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
 -10 -5 -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr
 5 10 15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
 20 25 30 35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
 40 45 50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
 55 60 65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser

79

75

80

Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
 85 90 95

Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
 100 105 110 115

Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
 120 125 130

Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
 135 140 145

Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
 150 155 160

Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
 165 170 175

Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
 180 185 190 195

Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
 200 205 210

Asn Asn Ile Gln Tyr Trp Ala Asn Gln
 215 220

<210> 15
 <211> 909
 <212> DNA
 <213> Bacillus intermedius

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<220>
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<220>
 <221> pro_peptide
 <222> (79)..(264)

<220>
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 <222> (265)..(909)

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 Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
 -85 -80 -75

gct tta agt gtg cct agt ttt gcc cat gcc aca tgg gat tca gta cta 90
 Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu
 -70 -65 -60

acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca 144
 Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
 -55 -50 -45

agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gac aaa gtg 192
 Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
 -40 -35 -30 -25

gat gat ctt tct tct act tct ggc gaa aaa gta aaa cca ctc tca aaa 240
 Asp Asp Leu Ser Ser Thr Ser Gly Glu Lys Val Lys Pro Leu Ser Lys
 -20 -15 -10

tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat gga ada 288
 Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Xaa
 -5 -1 1 5

aca aaa gta gca aac aca aga gtg gca coa tat aat tca att gct tat 336
 Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
 10 15 20

att aca ttt ggc ggc tca agc tgc acg ggg aca ctc att gcc cct aac 384
 Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
 25 30 35 40

aaa att ttg aca aac ggc cac tgc gtg tac aat aca gca tgg aga agt 432
 Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
 45 50 55

tat agt gca aaa gga tgg gtg tat cca ggc atg aac gat agt aca gcg 480
 Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
 60 65 70

gtg aat ggc tca gca aac atg acg gag ttc tat gta cca agc gga tat 528
 Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
 75 80 85

atc aat aca ggc gcg agc caa tat gat ttt gcc gtg atc aaa aca gat 576
 Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
 90 95 100

acg aac att ggc aat acg gtc ggt tac cgc tct atc cgt cag gtg aca 624
 Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
 105 110 115 120

aac tta act ggg aca acg att aaa att tct gga tat cca ggt gat aaa 672
 Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
 125 130 135
 atg ada tcg act ggc aag gtg tcg cad tgg gag atg tca ggt tct gtg 720
 Met Xaa Ser Thr Gly Lys Val Ser Xaa Trp Glu Met Ser Gly Ser Val
 140 145 150
 aca aga gaa gat aca aat ctc gca tac tat acg att gat aca ttt agc 768
 Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser
 155 160 165
 gga aat tca ggc tca gcg atg cta gat caa aat cad caa atc gtt ggg 816
 Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly
 170 175 180
 gtt cat aac gca ggg tat tca aac gga acg att aat ggc ggt cca aaa 864
 Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
 185 190 195 200
 gcg aca gct gcc ttt gtt gaa ttt atc aac tat gca aaa gcg caa 909
 Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
 205 210 215

<210> 16
 <211> 303
 <212> PRT
 <213> Bacillus intermedius

<220>
 <221> misc_feature
 <222> {8}..{8}
 <223> The 'Xaa' at location 8 stands for Lys, Arg, or Ile.

<220>
 <221> misc_feature
 <222> {138}..{138}
 <223> The 'Xaa' at location 138 stands for Lys, Arg, or Ile.

<220>
 <221> misc_feature
 <222> {145}..{145}
 <223> The 'Xaa' at location 145 stands for Gln, or His.

<220>
 <221> misc_feature
 <222> {189}..{189}
 <223> The 'Xaa' at location 189 stands for Gln, or His.

<400> 16

Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
 -85 -80 -75

Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu

-70

-65

-60

Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
-55 -50 -45

Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
-40 -35 -30 -25

Asp Asp Leu Ser Ser Thr Ser Gly Glu Lys Val Lys Pro Leu Ser Lys
-20 -15 -10

Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Xaa
-5 -1 1 5

Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
10 15 20

Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
25 30 35 40

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
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Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
125 130 135

Met Xaa Ser Thr Gly Lys Val Ser Xaa Trp Glu Met Ser Gly Ser Val
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly
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Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
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